

SEQUENCE LISTING

<110> Hitoshi, Yasumichi
Jenkins, Yonchu
Rigel Pharmaceuticals, Inc.

<120> Methods of Assaying for Cell Cycle Modulators

<130> 021044-003310PC

<140> US 10/510,903

<141> 2004-10-08

<150> US 10/123,568

<151> 2002-04-15

<150> US 10/123,731

<151> 2002-04-15

<150> US 60/373,366

<151> 2002-04-16

<150> WO PCT/US03/11867

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<170> PatentIn Ver. 2.1

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 (FANCA) (aldehyde dehydrogenase activity) cDNA

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 <213> Homo sapiens

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 (DDX9) (RNA helicase A, nuclear DNA helicase II,
 leukophysin), transcript variant 2

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 Lys Gln Pro Ala Ile Ile Ser Gln Leu Asp Pro Val Asn Glu Arg Met
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<220>
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 (cell surface kinase receptor) cDNA

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<211> 1367

<212> PRT

<213> Homo sapiens

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<223> insulin-like growth factor 1 receptor (IGF1R)
(cell surface kinase receptor)

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35 40 45

Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr Leu His Ile Leu Leu Ile
50 55 60

Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
65 70 75 80

Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
85 90 95

Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
100 105 110

Tyr	Asn	Tyr	Ala	Leu	Val	Ile	Phe	Glu	Met	Thr	Asn	Leu	Lys	Asp	Ile	115	120	125
Gly	Leu	Tyr	Asn	Leu	Arg	Asn	Ile	Thr	Arg	Gly	Ala	Ile	Arg	Ile	Glu	130	135	140
Lys	Asn	Ala	Asp	Leu	Cys	Tyr	Leu	Ser	Thr	Val	Asp	Trp	Ser	Leu	Ile	145	150	155
Leu	Asp	Ala	Val	Ser	Asn	Asn	Tyr	Ile	Val	Gly	Asn	Lys	Pro	Pro	Lys	165	170	175
Glu	Cys	Gly	Asp	Leu	Cys	Pro	Gly	Thr	Met	Glu	Glu	Lys	Pro	Met	Cys	180	185	190
Glu	Lys	Thr	Thr	Ile	Asn	Asn	Glu	Tyr	Asn	Tyr	Arg	Cys	Trp	Thr	Thr	195	200	205
Asn	Arg	Cys	Gln	Lys	Met	Cys	Pro	Ser	Thr	Cys	Gly	Lys	Arg	Ala	Cys	210	215	220
Thr	Glu	Asn	Asn	Glu	Cys	Cys	His	Pro	Glu	Cys	Leu	Gly	Ser	Cys	Ser	225	230	235
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Ala	Gly	Val	Cys	Val	Pro	Ala	Cys	Pro	Pro	Asn	Thr	Tyr	Arg	Phe	Glu	260	265	270
Gly	Trp	Arg	Cys	Val	Asp	Arg	Asp	Phe	Cys	Ala	Asn	Ile	Leu	Ser	Ala	275	280	285
Glu	Ser	Ser	Asp	Ser	Glu	Gly	Phe	Val	Ile	His	Asp	Gly	Glu	Cys	Met	290	295	300
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Cys	Ile	Pro	Cys	Glu	Gly	Pro	Cys	Pro	Lys	Val	Cys	Glu	Glu	Glu	Lys	325	330	335
Lys	Thr	Lys	Thr	Ile	Asp	Ser	Val	Thr	Ser	Ala	Gln	Met	Leu	Gln	Gly	340	345	350
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Thr	Gly	Tyr	Val	Lys	Ile	Arg	His	Ser	His	Ala	Leu	Val	Ser	Leu	Ser	385	390	395
Phe	Leu	Lys	Asn	Leu	Arg	Leu	Ile	Leu	Gly	Glu	Glu	Gln	Leu	Glu	Gly	405	410	415
Asn	Tyr	Ser	Phe	Tyr	Val	Leu	Asp	Asn	Gln	Asn	Leu	Gln	Gln	Leu	Trp	420	425	430

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 690 695 700
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Ser	Phe	Gly	Met	Val	Tyr	Glu	Gly	Val	Ala	Lys	Gly	Val	Val	Lys	Asp	1010	1015	1020
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<220>
 <223> ubiquitin-conjugating enzyme E2 variant 1
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<210> 12
 <211> 221
 <212> PRT
 <213> Homo sapiens

<220>
 <223> ubiquitin-conjugating enzyme E2 variant 1
 (UBE2V1), transcript variant 2

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Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe
20 25 30
Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg
35 40 45
Trp Val Thr Leu Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His
50 55 60
His Arg Ile His His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr
65 70 75 80
Thr Gly Val Lys Val Pro Arg Asn Phe Arg Leu Leu Glu Glu Leu Glu
85 90 95
Glu Gly Gln Lys Gly Val Gly Asp Gly Thr Val Ser Trp Gly Leu Glu
100 105 110
Asp Asp Glu Asp Met Thr Leu Thr Arg Trp Thr Gly Met Ile Ile Gly
115 120 125
Pro Pro Arg Thr Ile Tyr Glu Asn Arg Ile Tyr Ser Leu Lys Ile Glu
130 135 140
Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Phe Val Arg Phe Val Thr
145 150 155 160
Lys Ile Asn Met Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro
165 170 175
Arg Ala Ile Ser Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys
180 185 190
Val Val Leu Gln Glu Leu Arg Arg Leu Met Met Ser Lys Glu Asn Met
195 200 205
Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys Tyr Ser Asn
210 215 220

<210> 13
<211> 1506
<212> DNA
<213> Homo sapiens

<220>
<223> NADP+ dependent aldehyde dehydrogenase 1, soluble
(ALDH1) cDNA

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<210> 14

<211> 501

<212> PRT

<213> Homo sapiens

<220>

<223> NADP+ dependent aldehyde dehydrogenase 1, soluble
(ALDH1)

<400> 14

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Met Ser Ser Ser Gly Thr Pro Asp Leu Pro Val Leu Leu Thr Asp Leu
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```

```

Lys Ile Gln Tyr Thr Lys Ile Phe Ile Asn Asn Glu Trp His Asp Ser
      20             25             30

```

```

Val Ser Gly Lys Lys Phe Pro Val Phe Asn Pro Ala Thr Glu Glu Glu
      35             40             45

```

```

Leu Cys Gln Val Glu Glu Gly Asp Lys Glu Asp Val Asp Lys Ala Val
      50             55             60

```

```

Lys Ala Ala Arg Gln Ala Phe Gln Ile Gly Ser Pro Trp Arg Thr Met
      65             70             75             80

```

```

Asp Ala Ser Glu Arg Gly Arg Leu Leu Tyr Lys Leu Ala Asp Leu Ile
      85             90             95

```

```

Glu Arg Asp Arg Leu Leu Leu Ala Thr Met Glu Ser Met Asn Gly Gly
      100            105            110

```

```

Lys Leu Tyr Ser Asn Ala Tyr Leu Ser Asp Leu Ala Gly Cys Ile Lys
      115            120            125

```

```

Thr Leu Arg Tyr Cys Ala Gly Trp Ala Asp Lys Ile Gln Gly Arg Thr
      130            135            140

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Ile Pro Ile Asp Gly Asn Phe Phe Thr Tyr Thr Arg His Glu Pro Ile
      145            150            155            160

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Lys	Pro	Ala	Glu	Gln	Thr	Pro	Leu	Thr	Ala	Leu	His	Val	Ala	Ser	Leu	195	200	205	
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Tyr	Gly	Pro	Thr	Ala	Gly	Ala	Ala	Ile	Ser	Ser	His	Met	Asp	Ile	Asp	225	230	235	240
Lys	Val	Ala	Phe	Thr	Gly	Ser	Thr	Glu	Val	Gly	Lys	Leu	Ile	Lys	Glu	245	250	255	
Ala	Ala	Gly	Lys	Ser	Asn	Leu	Lys	Arg	Val	Thr	Leu	Glu	Leu	Gly	Gly	260	265	270	
Lys	Ser	Pro	Cys	Ile	Val	Leu	Ala	Asp	Ala	Asp	Leu	Asp	Asn	Ala	Val	275	280	285	
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Arg	Arg	Ser	Val	Glu	Arg	Ala	Lys	Lys	Tyr	Ile	Leu	Gly	Asn	Pro	Leu	325	330	335	
Thr	Pro	Gly	Val	Thr	Gln	Gly	Pro	Gln	Ile	Asp	Lys	Glu	Gln	Tyr	Asp	340	345	350	
Lys	Ile	Leu	Asp	Leu	Ile	Glu	Ser	Gly	Lys	Lys	Glu	Gly	Ala	Lys	Leu	355	360	365	
Glu	Cys	Gly	Gly	Gly	Pro	Trp	Gly	Asn	Lys	Gly	Tyr	Phe	Val	Gln	Pro	370	375	380	
Thr	Val	Phe	Ser	Asn	Val	Thr	Asp	Glu	Met	Arg	Ile	Ala	Lys	Glu	Glu	385	390	395	400
Ile	Phe	Gly	Pro	Val	Gln	Gln	Ile	Met	Lys	Phe	Lys	Ser	Leu	Asp	Asp	405	410	415	
Val	Ile	Lys	Arg	Ala	Asn	Asn	Thr	Phe	Tyr	Gly	Leu	Ser	Ala	Gly	Val	420	425	430	
Phe	Thr	Lys	Asp	Ile	Asp	Lys	Ala	Ile	Thr	Ile	Ser	Ser	Ala	Leu	Gln	435	440	445	
Ala	Gly	Thr	Val	Trp	Val	Asn	Cys	Tyr	Gly	Val	Val	Ser	Ala	Gln	Cys	450	455	460	
Pro	Phe	Gly	Gly	Phe	Lys	Met	Ser	Gly	Asn	Gly	Arg	Glu	Leu	Gly	Glu	465	470	475	480

Tyr Gly Phe His Glu Tyr Thr Glu Val Lys Thr Val Thr Val Lys Ile
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Ser Gln Lys Asn Ser
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<210> 15
 <211> 2282
 <212> DNA
 <213> Homo sapiens

<220>
 <223> similar to pyruvate kinase, muscle cDNA

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<210> 16
 <211> 531
 <212> PRT
 <213> Homo sapiens

<220>

<223> similar to pyruvate kinase, muscle

<400> 16

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Gln	Leu	His	Ala	Ala	Met	Ala	Asp	Thr	Phe	Leu	Glu	His	Met	Cys	Arg
			20					25					30		
Leu	Asp	Ile	Asp	Ser	Pro	Pro	Ile	Thr	Ala	Arg	Asn	Thr	Gly	Ile	Ile
		35					40					45			
Cys	Thr	Ile	Gly	Pro	Ala	Ser	Arg	Ser	Val	Glu	Thr	Leu	Lys	Glu	Met
	50					55					60				
Ile	Lys	Ser	Gly	Met	Asn	Val	Ala	Arg	Leu	Asn	Phe	Ser	His	Gly	Thr
65					70					75				80	
His	Glu	Tyr	His	Ala	Glu	Thr	Ile	Lys	Asn	Val	Arg	Thr	Ala	Thr	Glu
				85					90					95	
Ser	Phe	Ala	Ser	Asp	Pro	Ile	Leu	Tyr	Arg	Pro	Val	Ala	Val	Ala	Leu
			100					105					110		
Asp	Thr	Lys	Gly	Pro	Glu	Ile	Arg	Thr	Gly	Leu	Ile	Lys	Gly	Ser	Gly
		115					120					125			
Thr	Ala	Glu	Val	Glu	Leu	Lys	Lys	Gly	Ala	Thr	Leu	Lys	Ile	Thr	Leu
	130					135					140				
Asp	Asn	Ala	Tyr	Met	Glu	Lys	Cys	Asp	Glu	Asn	Ile	Leu	Trp	Leu	Asp
145					150					155					160
Tyr	Lys	Asn	Ile	Cys	Lys	Val	Val	Glu	Val	Gly	Ser	Lys	Ile	Tyr	Val
			165						170				175		
Asp	Asp	Gly	Leu	Ile	Ser	Leu	Gln	Val	Lys	Gln	Lys	Gly	Ala	Asp	Phe
			180					185					190		
Leu	Val	Thr	Glu	Val	Glu	Asn	Gly	Gly	Ser	Leu	Gly	Ser	Lys	Lys	Gly
		195					200					205			
Val	Asn	Leu	Pro	Gly	Ala	Ala	Val	Asp	Leu	Pro	Ala	Val	Ser	Glu	Lys
	210					215					220				
Asp	Ile	Gln	Asp	Leu	Lys	Phe	Gly	Val	Glu	Gln	Asp	Val	Asp	Met	Val
225					230					235				240	
Phe	Ala	Ser	Phe	Ile	Arg	Lys	Ala	Ser	Asp	Val	His	Glu	Val	Arg	Lys
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Lys Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala
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 Gly Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys
 325 330 335
 Lys Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val
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 Leu Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly
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 Asp Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu
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 Ala Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg
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 Val Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr
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 Lys Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala
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 Pro Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His
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 Leu Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu
 465 470 475 480
 Ala Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val
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 Pro Val Pro
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<210> 17

<211> 2631

<212> DNA

<213> Homo sapiens

<220>

<223> glucose-6-phosphate dehydrogenase (G6PD) cDNA

<400> 17

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<210> 18

<211> 515

<212> PRT

<213> Homo sapiens

<220>

<223> glucose-6-phosphate dehydrogenase (G6PD)

<400> 18

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Arg Glu Glu Leu Phe Gln Gly Asp Ala Phe His Gln Ser Asp Thr His
20 25 30

Ile Phe Ile Ile Met Gly Ala Ser Gly Asp Leu Ala Lys Lys Lys Ile
35 40 45

Tyr Pro Thr Ile Trp Trp Leu Phe Arg Asp Gly Leu Leu Pro Glu Asn
50 55 60

Thr	Phe	Ile	Met	Gly	Tyr	Ala	Arg	Ser	Arg	Leu	Thr	Val	Ala	Asp	Ile	65	70	75	80
Arg	Lys	Gln	Ser	Glu	Pro	Phe	Phe	Lys	Ala	Thr	Pro	Glu	Glu	Lys	Leu	85	90	95	
Lys	Leu	Glu	Asp	Phe	Phe	Ala	Arg	Asn	Ser	Tyr	Val	Ala	Gly	Gln	Tyr	100	105	110	
Asp	Asp	Ala	Ala	Ser	Tyr	Gln	Arg	Leu	Asn	Ser	His	Met	Asp	Ala	Leu	115	120	125	
His	Leu	Gly	Ser	Gln	Ala	Asn	Arg	Leu	Phe	Tyr	Leu	Ala	Leu	Pro	Pro	130	135	140	
Thr	Val	Tyr	Glu	Ala	Val	Thr	Lys	Asn	Ile	His	Glu	Ser	Cys	Met	Ser	145	150	155	160
Gln	Ile	Gly	Trp	Asn	Arg	Ile	Ile	Val	Glu	Lys	Pro	Phe	Gly	Arg	Asp	165	170	175	
Leu	Gln	Ser	Ser	Asp	Arg	Leu	Ser	Asn	His	Ile	Ser	Ser	Leu	Phe	Arg	180	185	190	
Glu	Asp	Gln	Ile	Tyr	Arg	Ile	Asp	His	Tyr	Leu	Gly	Lys	Glu	Met	Val	195	200	205	
Gln	Asn	Leu	Met	Val	Leu	Arg	Phe	Ala	Asn	Arg	Ile	Phe	Gly	Pro	Ile	210	215	220	
Trp	Asn	Arg	Asp	Asn	Ile	Ala	Cys	Val	Ile	Leu	Thr	Phe	Lys	Glu	Pro	225	230	235	240
Phe	Gly	Thr	Glu	Gly	Arg	Gly	Gly	Tyr	Phe	Asp	Glu	Phe	Gly	Ile	Ile	245	250	255	
Arg	Asp	Val	Met	Gln	Asn	His	Leu	Leu	Gln	Met	Leu	Cys	Leu	Val	Ala	260	265	270	
Met	Glu	Lys	Pro	Ala	Ser	Thr	Asn	Ser	Asp	Asp	Val	Arg	Asp	Glu	Lys	275	280	285	
Val	Lys	Val	Leu	Lys	Cys	Ile	Ser	Glu	Val	Gln	Ala	Asn	Asn	Val	Val	290	295	300	
Leu	Gly	Gln	Tyr	Val	Gly	Asn	Pro	Asp	Gly	Glu	Gly	Glu	Ala	Thr	Lys	305	310	315	320
Gly	Tyr	Leu	Asp	Asp	Pro	Thr	Val	Pro	Arg	Gly	Ser	Thr	Thr	Ala	Thr	325	330	335	
Phe	Ala	Ala	Val	Val	Leu	Tyr	Val	Glu	Asn	Glu	Arg	Trp	Asp	Gly	Val	340	345	350	
Pro	Phe	Ile	Leu	Arg	Cys	Gly	Lys	Ala	Leu	Asn	Glu	Arg	Lys	Ala	Glu	355	360	365	
Val	Arg	Leu	Gln	Phe	His	Asp	Val	Ala	Gly	Asp	Ile	Phe	His	Gln	Gln	370	375	380	

Cys Lys Arg Asn Glu Leu Val Ile Arg Val Gln Pro Asn Glu Ala Val
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 Tyr Thr Lys Met Met Thr Lys Lys Pro Gly Met Phe Phe Asn Pro Glu
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 420 425 430
 Leu Pro Asp Ala Tyr Glu Arg Leu Ile Leu Asp Val Phe Cys Gly Ser
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 Gln Met His Phe Val Arg Ser Asp Glu Leu Arg Glu Ala Trp Arg Ile
 450 455 460
 Phe Thr Pro Leu Leu His Gln Ile Glu Leu Glu Lys Pro Lys Pro Ile
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 His Lys Leu
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<210> 19
 <211> 1564
 <212> DNA
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<220>
 <223> HCDR-3, proliferation-associated 2G4 (PA2G4)
 (protease) cDNA

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<212> PRT

<213> Homo sapiens

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 (protease)

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Val	Val	Thr	Lys	Tyr	Lys	Met	Gly	Gly	Asp	Ile	Ala	Asn	Arg	Val	Leu	20	25	30	
Arg	Ser	Leu	Val	Glu	Ala	Ser	Ser	Ser	Gly	Val	Ser	Val	Leu	Ser	Leu	35	40	45	
Cys	Glu	Lys	Gly	Asp	Ala	Met	Ile	Met	Glu	Glu	Thr	Gly	Lys	Ile	Phe	50	55	60	
Lys	Lys	Glu	Lys	Glu	Met	Lys	Lys	Gly	Ile	Ala	Phe	Pro	Thr	Ser	Ile	65	70	75	80
Ser	Val	Asn	Asn	Cys	Val	Cys	His	Phe	Ser	Pro	Leu	Lys	Ser	Asp	Gln	85	90	95	
Asp	Tyr	Ile	Leu	Lys	Glu	Gly	Asp	Leu	Val	Lys	Ile	Asp	Leu	Gly	Val	100	105	110	
His	Val	Asp	Gly	Phe	Ile	Ala	Asn	Val	Ala	His	Thr	Phe	Val	Val	Asp	115	120	125	
Val	Ala	Gln	Gly	Thr	Gln	Val	Thr	Gly	Arg	Lys	Ala	Asp	Val	Ile	Lys	130	135	140	
Ala	Ala	His	Leu	Cys	Ala	Glu	Ala	Ala	Leu	Arg	Leu	Val	Lys	Pro	Gly	145	150	155	160
Asn	Gln	Asn	Thr	Gln	Val	Thr	Glu	Ala	Trp	Asn	Lys	Val	Ala	His	Ser	165	170	175	
Phe	Asn	Cys	Thr	Pro	Ile	Glu	Gly	Met	Leu	Ser	His	Gln	Leu	Lys	Gln	180	185	190	
His	Val	Ile	Asp	Gly	Glu	Lys	Thr	Ile	Ile	Gln	Asn	Pro	Thr	Asp	Gln	195	200	205	
Gln	Lys	Lys	Asp	His	Glu	Lys	Ala	Glu	Phe	Glu	Val	His	Glu	Val	Tyr	210	215	220	
Ala	Val	Asp	Val	Leu	Val	Ser	Ser	Gly	Glu	Gly	Lys	Ala	Lys	Asp	Ala	225	230	235	240


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<211> 558

<212> PRT

<213> Homo sapiens

<220>

<223> DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21
(DDX21) (RNA helicase II)

<400> 22

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Met Lys Lys Gly Glu Thr Leu Arg Lys Gln Thr Glu Glu Lys Glu Lys
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Lys Glu Lys Pro Lys Ser Asp Lys Thr Glu Glu Ile Ala Glu Glu Glu
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Glu Thr Val Phe Pro Lys Ala Lys Gln Val Lys Lys Lys Ala Glu Pro
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Ser Glu Val Asp Met Asn Ser Pro Lys Ser Lys Lys Ala Lys Lys Lys
      65                      70                      75                      80

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Glu	Glu	Pro	Ser	Gln	Asn	Asp	Ile	Ser	Pro	Lys	Thr	Lys	Ser	Leu	Arg	85	90	95
Lys	Lys	Lys	Glu	Pro	Ile	Glu	Lys	Lys	Val	Val	Ser	Ser	Lys	Thr	Lys	100	105	110
Lys	Val	Thr	Lys	Asn	Glu	Glu	Pro	Ser	Glu	Glu	Glu	Ile	Asp	Ala	Pro	115	120	125
Lys	Pro	Lys	Lys	Met	Lys	Lys	Glu	Lys	Glu	Met	Asn	Gly	Glu	Thr	Arg	130	135	140
Glu	Lys	Ser	Pro	Lys	Leu	Lys	Asn	Gly	Phe	Pro	His	Pro	Glu	Pro	Asp	145	150	155
Cys	Asn	Pro	Ser	Glu	Ala	Ala	Ser	Glu	Glu	Ser	Asn	Ser	Glu	Ile	Glu	165	170	175
Gln	Glu	Ile	Pro	Val	Glu	Gln	Lys	Glu	Gly	Ala	Phe	Ser	Asn	Phe	Pro	180	185	190
Ile	Ser	Glu	Glu	Thr	Ile	Lys	Leu	Leu	Lys	Gly	Arg	Gly	Val	Thr	Phe	195	200	205
Leu	Phe	Pro	Ile	Gln	Ala	Lys	Thr	Phe	His	His	Val	Tyr	Ser	Gly	Lys	210	215	220
Asp	Leu	Ile	Ala	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Phe	Ser	Phe	225	230	235
Ala	Ile	Pro	Leu	Ile	Glu	Lys	Leu	His	Gly	Glu	Leu	Gln	Asp	Arg	Lys	245	250	255
Arg	Gly	Arg	Ala	Pro	Gln	Val	Leu	Val	Leu	Ala	Pro	Thr	Arg	Glu	Leu	260	265	270
Ala	Asn	Gln	Val	Ser	Lys	Asp	Phe	Ser	Asp	Ile	Thr	Lys	Lys	Leu	Ser	275	280	285
Val	Ala	Cys	Phe	Tyr	Gly	Gly	Thr	Pro	Tyr	Gly	Gly	Gln	Phe	Glu	Arg	290	295	300
Met	Arg	Asn	Gly	Ile	Asp	Ile	Leu	Val	Gly	Thr	Pro	Gly	Arg	Ile	Lys	305	310	315
Asp	His	Ile	Gln	Asn	Gly	Lys	Leu	Asp	Leu	Thr	Lys	Leu	Lys	His	Val	325	330	335
Val	Leu	Asp	Glu	Val	Asp	Gln	Met	Leu	Asp	Met	Gly	Phe	Ala	Asp	Gln	340	345	350
Val	Glu	Glu	Ile	Leu	Ser	Val	Ala	Tyr	Lys	Lys	Asp	Ser	Glu	Asp	Asn	355	360	365
Pro	Gln	Thr	Leu	Leu	Phe	Ser	Ala	Thr	Cys	Pro	His	Trp	Val	Phe	Asn	370	375	380
Val	Ala	Lys	Lys	Tyr	Met	Lys	Ser	Thr	Tyr	Glu	Gln	Val	Asp	Leu	Ile	385	390	395

Gly Lys Lys Thr Gln Lys Thr Ala Ile Thr Val Glu His Leu Ala Ile
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 Lys Cys His Trp Thr Gln Arg Ala Ala Val Ile Gly Asp Val Ile Arg
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 Val Tyr Ser Gly His Gln Gly Arg Thr Ile Ile Phe Cys Glu Thr Lys
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 Ser Pro Pro Lys Gly Cys Arg Val Leu His Ser Ser Ile Arg Ala Asp
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<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<223> ARK2, serine/threonine kinase 15 (STK15) cDNA

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 <213> Homo sapiens

<220>
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 Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln
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 Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu Asn Asn Thr Gln
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 Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
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 Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys Lys Arg Gln Trp
 115 120 125
 Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys Phe
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 145 150 155 160
 Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala Gly Val Glu His
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Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr Arg Val Tyr Leu
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 Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr Ile Thr Glu Leu
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 245 250 255
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 <212> DNA
 <213> Homo sapiens

<220>
 <223> similar to transmembrane 4 superfamily member 1
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ccaggacaga gccacaatct tcctctatct cattgtaatt tatatatctt acttgatttc 780
atctgtaaaa ctttgtatta gtgtaacata ctccccacag tctactttta caaacgcctg 840
taaagactgg catcttcaca ggatgtcagt gtttaaattt agtaaacttc tttttgttt 900
gtttatttgt ttttgttttt tttttaggaa tgaggaaaca aaccaccctc tgggggtagt 960
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agttgctttt tataagacca agaaggagaa aatccgacaa cctggaaaga tttttgtttt 1140
cactgcttgt atgatgtttc ccattcatac acctataaat ctctaacaag aggccctttg 1200
aactgccttg tgttctgtga gaaacaaata tttacttaga gtggaaggac tgattgagaa 1260
tgttccaatc caaatgaatg catcacaact tacaatgctg ctcatgttg tgagtactat 1320
gagattcaaa tttttctaac atatggaaag ccttttgtcc tccaaagatg agtactaggg 1380
atcatgtgtt taaaaaaaaa aaaggctacg atgactgggc aagaagaaag atgggaaact 1440
gaataaagca gttgatcagc atcattggaa catggggacg agtgacggca ggaggaccac 1500
gaggaaatac cctcaaaact aacttgttta caacaaaata aagtattcac tacgaaaaaa 1560
aaaaaaaaaa aaaaaaaaaa aaaa 1584

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<210> 26

<211> 202

<212> PRT

<213> Homo sapiens

<220>

<223> similar to transmembrane 4 superfamily member 1
(TM4 SF1)

<400> 26

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Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser Leu Val Gly
  1              5              10              15

Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr Phe Pro Asn
      20              25              30

Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
      35              40              45

Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
      50              55              60

Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
      65              70              75              80

His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
      85              90              95

Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
      100             105             110

Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
      115             120             125

Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser
      130             135             140

Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val
      145             150             155             160

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Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu
165 170 175

Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe
180 185 190

Cys Cys Ser His Gln Gln Gln Tyr Asp Cys
195 200

<210> 27

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<223> excision repair cross-complementing rodent repair
deficiency, complementation group 1 (ERCC1) cDNA

<400> 27

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ccaagaccag caggtgaggc ctcgcggcgc tgaaaccgtg aggcccggac cacaggctcc 60
agatggaccc tgggaaggac aaagaggggg tgccccagcc ctcagggccg ccagcaagga 120
agaaatttgt gatacccctc gacgaggatg aggtccctcc tggagtggcc aagcccttat 180
tccgatctac acagagcctt cccactgtgg acacctcggc ccaggcggcc cctcagacct 240
acgccgaata tgccatctca cagcctctgg aaggggctgg ggccacgtgc cccacagggt 300
cagagcccct ggcaggagag acgccaacc aggcctgaa acccggggca aaatccaaca 360
gcatcattgt gagccctcgg cagaggggca atcccgtact gaagtctgtg cgcaatgtgc 420
cctgggaatt tggcgacgta attcccgaact atgtgctggg ccagagcacc tgtgccctgt 480
tcctcagcct ccgctaccac aacctgcacc cagactacat ccatgggcgg ctgcagagcc 540
tggggaagaa cttcgccttg cgggtcctgc ttgtccaggt ggatgtgaaa gatccccagc 600
aggccctcaa ggagctggct aagatgtgta tcctggccga ctgcacattg atcctcgctt 660
ggagccccga ggaagctggg cggtaacctg agacctacaa ggcctatgag cagaaaccag 720
cggacctcct gatggagaag ctagagcagg acttcgtctc ccgggtgact gaatgtctga 780
ccaccgtgaa gtcagtcaac aaaacggaca gtcagaccct cctgaccaca tttggatctc 840
tggaacagct catcgccgca tcaagagaag atctggcctt atgcccaggc ctggggcctc 900
agaaagcccg gaggtgttt gatgtcctgc acgagccctt cttgaaagta ccctgatgac 960
cccagctgcc aaggaaaccc ccagtgtaat aataaatcgt cctcccaggc caggctcctg 1020
ctggc                                     1025

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<210> 28

<211> 297

<212> PRT

<213> Homo sapiens

<220>

<223> excision repair cross-complementing rodent repair
deficiency, complementation group 1 (ERCC1)

<400> 28

Met Asp Pro Gly Lys Asp Lys Glu Gly Val Pro Gln Pro Ser Gly Pro
1 5 10 15

Pro Ala Arg Lys Lys Phe Val Ile Pro Leu Asp Glu Asp Glu Val Pro
20 25 30

Pro Gly Val Ala Lys Pro Leu Phe Arg Ser Thr Gln Ser Leu Pro Thr
35 40 45

Val Asp Thr Ser Ala Gln Ala Ala Pro Gln Thr Tyr Ala Glu Tyr Ala
50 55 60

Ile Ser Gln Pro Leu Glu Gly Ala Gly Ala Thr Cys Pro Thr Gly Ser
 65 70 75 80
 Glu Pro Leu Ala Gly Glu Thr Pro Asn Gln Ala Leu Lys Pro Gly Ala
 85 90 95
 Lys Ser Asn Ser Ile Ile Val Ser Pro Arg Gln Arg Gly Asn Pro Val
 100 105 110
 Leu Lys Phe Val Arg Asn Val Pro Trp Glu Phe Gly Asp Val Ile Pro
 115 120 125
 Asp Tyr Val Leu Gly Gln Ser Thr Cys Ala Leu Phe Leu Ser Leu Arg
 130 135 140
 Tyr His Asn Leu His Pro Asp Tyr Ile His Gly Arg Leu Gln Ser Leu
 145 150 155 160
 Gly Lys Asn Phe Ala Leu Arg Val Leu Leu Val Gln Val Asp Val Lys
 165 170 175
 Asp Pro Gln Gln Ala Leu Lys Glu Leu Ala Lys Met Cys Ile Leu Ala
 180 185 190
 Asp Cys Thr Leu Ile Leu Ala Trp Ser Pro Glu Glu Ala Gly Arg Tyr
 195 200 205
 Leu Glu Thr Tyr Lys Ala Tyr Glu Gln Lys Pro Ala Asp Leu Leu Met
 210 215 220
 Glu Lys Leu Glu Gln Asp Phe Val Ser Arg Val Thr Glu Cys Leu Thr
 225 230 235 240
 Thr Val Lys Ser Val Asn Lys Thr Asp Ser Gln Thr Leu Leu Thr Thr
 245 250 255
 Phe Gly Ser Leu Glu Gln Leu Ile Ala Ala Ser Arg Glu Asp Leu Ala
 260 265 270
 Leu Cys Pro Gly Leu Gly Pro Gln Lys Ala Arg Arg Leu Phe Asp Val
 275 280 285
 Leu His Glu Pro Phe Leu Lys Val Pro
 290 295

<210> 29

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<223> cell tracker assay functional hit from retroviral
screen FANCA partial cDNA

<400> 29

ccagtgtgct ggaaaggagg aagatatacct ggctggcact ctttcagttg acagagagtg 60
 acctcaggct ggggcggctc ctctccgtg tggccccgga tcagcacacc aggctgctgc 120
 ctttcgcttt ttacagtctt ctctctact tccatgaaga cgcggtttc cagcacagtgc 180
 g 181

<210> 30
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<223> cell tracker assay functional hit from retroviral
screen DDX9 partial cDNA

<400> 30
ccagtgtgct ggaaagcgcc acctcctctt cctgtgccaa agtagccagt tccataggcc 60
cccctaccac cwcctcgctg gaatccccc gatcctctgt agcctccact aggccctctg 120
tagtctcctc cagagttgcc tctaaagcca cctcgggaga ctctctata gcctccacca 180
acacctgcac catatcctgc ccgaaaggag ttggcgctgc caccatagcc tccgctacca 240
tagcctccac tgctatagcc accgcatagc ctccaccact gtaactagaa cctccccctt 300
tatatccgct tccattgtcg tatcggggcca tcttgggagg acgtggacca tctccatgcc 360
gtgtactgcc aatcataagg ttgataccag cagctgaggg tctagagatc tgacggatca 420
tgttcagcat acgttcattt acgggggtcca actggctgat gatagcaggt tgtttggtta 480
cttcaacaac caaagcctcc atggctgccc ggagaccagt gatacaggca gcagcttcat 540
gagatatttg cagtttaatc cagtcattca caagcacaat ctgcccactt tccagcacag 600
tgg 603

<210> 31
<211> 145
<212> DNA
<213> Homo sapiens

<220>
<223> cell tracker assay functional hit from retroviral
screen IGF1R partial cDNA

<400> 31
ccagtgtggt ggaaagggag agaactgtca tttctaacct tcggcctttc acattgtacc 60
gcatcgatat ccacagctgc aaccacgagg ctgagaagct gggctgcagc gcctccaact 120
tcgtctttgc tttccagcac agtgg 145

<210> 32
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<223> cell tracker assay functional hit from retroviral
screen UBEV2V1 partial cDNA

<400> 32
ccagtgtgct ggaaagggtg ttctgggtat ttaggtccac attctatctt aaggctgtat 60
attcgggtttt cataaattgt tcttggaggc ccaattatca tccctgtcca tcttgtaaga 120
tgtcatgtct tcgtcatctt ctgaccccca gctaactgtg ccatctccta ctctttctg 180
gccttcttcg agattcctcc aacagtcgga aattgcgagg gactttatac atcccagacc 240
cgtgggtggct gccctttcca gcacactgg 269

<210> 33
<211> 499
<212> DNA
<213> Homo sapiens

<220>
 <223> cell tracker assay functional hit from retroviral
 screen aldehyde dehydrogenase partial cDNA

<400> 33
 ccagtgtgct ggaaaggagc aaactcctct cactgctctc cacgtggcat ctttaataaa 60
 agaggcaggg tttcctcctg gagtagtgaa tattgttcct ggttatgggc ctacagcagg 120
 ggcagccatt tcttctcaca tggatataga caaagtagcc ttcacaggat caacagaggt 180
 tggcaagttg atcaaagaag ctgccgggaa aagcaatctg aagaggggtga ccctggagct 240
 tggaggaaaag agcccttgca ttgtgttagc tgatgccgac ttggacaatg ctgttgaatt 300
 tgcacaccat ggggtattct accaccaggg ccagtgttgt atagccgcat ccaggatttt 360
 tgtggaagaa tcaatttatg atgagttttg ttcgaaggag tgttgagcgg gctaagaacg 420
 tataccttg gaaacatcct ctgacccag gagtcactca aaggccctca gattgacaag 480
 gactttccag acacagtgg 499

<210> 34
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <223> cell tracker assay functional hit from retroviral
 screen pyruvate dehydrogenase partial cDNA

<400> 34
 ccagtgtgct ggaaaggctg ccacttcca ccaccttgca gatgttcttg tagtccagcc 60
 acaggatggt ctcgtcacac ttttccatgt aggcgttata cagcgtgatt ttgagagtgg 120
 ctcccttctt cagctccacc tctgcagtgc cgctgccctt gatgagccca gttcggatct 180
 caggtccttt agtgtctaga gccacagcaa cgggcccggta gaggatgggg tcagaagcaa 240
 agctttccgt ggctgtgctg acattcttga tgggtctcgc atggtactca tgagttccat 300
 gagagaagtt cagacgagcc acattcattc cagacttaat catctccttc aacgtctcca 360
 ctggatcggg aagctgggac aatggtacag atgatgccag tggtccgggc tttccagcac 420
 agtgg 425

<210> 35
 <211> 238
 <212> DNA
 <213> Homo sapiens

<220>
 <223> cell tracker assay functional hit from retroviral
 screen G6PD partial cDNA

<220>
 <221> modified_base
 <222> (1)..(238)
 <223> n = g, a, c or t

<400> 35
 ccagtgtgct ggaaactttc cagttctcca tggccaccan acacagcatc tgcagttaggt 60
 ggttctgcat cacgtcccgg atgatcccaa attcatcgaa atagcccccg cgaccctcag 120
 tgccaaaggg ctccctgaag gtgaggataa cgcaggcgat gttgtcccgg ttccanattg 180
 ggccgaagat cctgttggca aatctcagca ccatgaggtt ctctttccag cacagtgg 238

<210> 36
 <211> 491
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G3-2D8 sequence
 with C-terminus of GFP, partial BAP-1 sequence

<220>
 <221> modified_base
 <222> (69)
 <223> n = g, a, c or t

<400> 36
 gagttcgtga cgcgccgccc gatacactctc ggcatggacg agctgtacaa ggaggaggcc 60
 gccaaaggcng gtggcagcgg tggctccagt gtgctggaaa gctaagggca gagttggtgt 120
 tctgcacgtc atcctctcgt catcctcata gtcacacctca tcatctgagt actgctgggg 180
 tggggcggact ggaactcggc tgcggccac acctgccgcc aggtcttctt cctcctgcat 240
 ggggggacttg gcataattgt gattgtctag aaaggccggc agccgctgga caatgggagt 300
 ggggttgggg tgaaccccat tgaggctgct gcctggaggc taccactagc ttgggtttgt 360
 tgggagggct gtgggatggg gcttgtgcgc atgaaccagc cgcctcctcg caccatctgt 420
 gtggttgccc tcagaggctg caggggccct gtttgcttcc agcaccagcg gggaaccttc 480
 cagcacagtg g 491

<210> 37
 <211> 34
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G3-2D8 sequence
 with C-terminus of GFP, partial BAP-1 sequence

<400> 37
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 1 5 10 15
 Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu
 20 25 30
 Glu Ser

<210> 38
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:BstXI linker

<400> 38
 ccagtgtgct ggaaaag 16

<210> 39
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:BstXI linker

<400> 39
ctttccagca cagtgg

16

<210> 40
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<223> G1-2635 sequence, partial NP95 sequence

<400> 40
Ala Glu Gln Ser Cys Asp Gln Lys Leu Thr Asn Thr Asn Arg Ala Leu
1 5 10 15
Ala Leu Asn Cys Phe Ala Pro Ile Asn Asp Gln Glu Gly Ala Glu Ala
20 25 30
Lys Asp Trp Arg Ser Gly Lys Pro Val Arg Val Val Arg Asn Val Lys
35 40 45
Gly Gly Lys Asn Ser Lys Tyr Ala Pro Ala Glu Gly Asn Arg Tyr Asp
50 55 60
Gly Ile Tyr Lys Val Val Lys Tyr Trp Pro Glu Lys Gly Lys Ser Gly
65 70 75 80
Phe Leu Val Trp Arg Tyr Leu Leu Arg Arg Asp Asp Asp Glu Pro Gly
85 90 95
Pro Trp Thr Lys Glu Gly Lys Asp Arg Ile Lys Lys Leu Gly Leu Thr
100 105 110
Met Gln Tyr Pro Glu Gly Tyr Leu Glu Ala Leu Ala Asn Arg Glu Arg
115 120 125
Glu Lys Glu Asn Ser Lys Arg Glu
130 135

<210> 41
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<223> G2-2F3 sequence, partial FANCA sequence

<400> 41
Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln Leu Thr Glu Ser Asp Leu
1 5 10 15
Arg Leu Gly Arg Leu Leu Leu Arg Val Ala Pro Asp Gln His Thr Arg
20 25 30
Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu Ser Tyr Phe His Glu Asp
35 40 45

Ala

<210> 42
 <211> 552
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2H6 sequence
 with C-terminus of GFP, partial DDX9 sequence

<400> 42
 gagttcgtga cgcgcgcgcg gatcactctc ggcattggacg agctgtacaa ggaggaggcc 60
 gccaaggccg gtggcagcgg tggctccagt gtgctggaaa gcgccacctc ctcttccttg 120
 tccaaagtag ccagttccat aggccccct accacctcct cgctggaatc cccagatcc 180
 tctgtagcct ccactaggcc ctctgtagtc tcctccagag ttgcctctaa agccacctcg 240
 ggagactcct ctatagcctc caccaacacc tgcaccatat cctgcccgaaggagggtggc 300
 gctgccacca tagcctccgc taccatagcc tccactgcta tagccaccgc atagcctcca 360
 ccactgtaac tagaacctcc ctttctatat ccgcttccat tgctgtatcg ggccatcttg 420
 ggaggacgtg gaccatctcc atgccgtgta ctgccaatca taagggtgat accagcagct 480
 gaggggtctac agatctgacg gatcatgttc agcatacgtt catttacggg gtccaactgg 540
 ctgatgatag ca 552

<210> 43
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2H6 sequence
 with C-terminus of GFP, partial DDX9 sequence

<400> 43
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 1 5 10 15
 Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu
 20 25 30
 Glu Ser Ala Thr Ser Ser Ser Leu Ser Lys Val Ala Ser Ser Ile Gly
 35 40 45
 Pro Pro Thr Thr Ser Ser Leu Glu Ser Pro Arg Ser Ser Val Ala Ser
 50 55 60
 Thr Arg Pro Ser Val Val Ser Ser Arg Val Ala Ser Lys Ala Thr Ser
 65 70 75 80
 Gly Asp Ser Ser Ile Ala Ser Thr Asn Thr Cys Thr Ile Ser Cys Pro
 85 90 95
 Lys Gly Val Gly Ala Ala Thr Ile Ala Ser Ala Thr Ile Ala Ser Thr
 100 105 110
 Ala Ile Ala Thr Ala
 115

<210> 44
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <223> G3-2H2_1 sequence, partial IGF1R sequence

<400> 44
 Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg Ile
 1 5 10 15
 Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser Ala
 20 25 30
 Ser Asn Phe Val Phe Ala
 35

<210> 45
 <211> 347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 45
 gagttcgtga ccgccgccgg gatcactctc ggcattggacg agctgtacaa ggaggaggcc 60
 gccaaggccg gtggcagcgg tggctccagt gtgctggaaa ggtgcttctg ggtatttagg 120
 tccacattct attttaaggc tgtatatctg gttttcataa attgttcttg gaggcccaat 180
 tatcatccct gtccatcttg taagtgtcat gtcttcgtca tcttctagac cccagctaac 240
 tgtgccatct cctactcctt tctggccttc ttcgagttct tccaacagtc ggaaattgcg 300
 agggactttt actcccgagc ccgtggtggc tctttccagc acagtgg 347

<210> 46
 <211> 75
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 46
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 1 5 10 15
 Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu
 20 25 30
 Glu Arg Cys Phe Trp Val Phe Arg Ser Thr Phe Tyr Phe Lys Ala Val
 35 40 45
 Tyr Ser Val Phe Ile Asn Cys Ser Trp Arg Pro Asn Tyr His Pro Cys
 50 55 60
 Pro Ser Cys Lys Cys His Val Phe Val Ile Phe
 65 70 75

<210> 47
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<223> portion of G3_2H2 sequence

<400> 47
ggcagccacc acgggctcgg gagtaaaagt ccctcgcaat ttccgactgt tggaagaact 60
cgaagaaggc cagaaaggag taggagatgg cacagttagc tggggcttag aagatgacga 120
agacatgaca cttacaagat ggacagggat gataattggg cctccaagaa caattta 177

<210> 48
<211> 198
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v1 alternatively spliced
transcript

<400> 48
ggcacgaggg cgacgcaaga tggcagccac cacgggctcg ggagtaaaag tccctcgcaa 60
tttccgactg ttggaagaac tcgaagaagg ccagaaagga gtaggagatg gcacagttag 120
ctgggggtcta gaagatgacg aagacatgac acttacaaga tggacaggga tgataattgg 180
gcctccaaga acaattta 198

<210> 49
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v1_2 alternatively spliced
transcript

<400> 49
gtcatcctgc cacgtaaaca ccacgcacac caccacgtct caccacacga gacctacttc 60
tgcacacca caggagtaaa agtcctcgc aatttcgcac tggtggaaga ac 112

<210> 50
<211> 113
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v1_1 alternatively spliced
transcript

<400> 50
aagcgtctta cctgaagtca caaagcaaac tgagtgatga aggaagactt gaacctagaa 60
aatttcactg caaaggagat aaaagtcct cgcaatttcg actggttgaa gaa 113

<210> 51
<211> 192
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v1Bs alternatively spliced
transcript

<400> 51
atggcctaca agttccgcac agtggttacag ccctggagta aaagtccctc gcaatttccg 60
actgttgga gaactcgaag aaggccagaa aggagtagga gatggcacag ttagctgggg 120
tctagaagat gacgaagaca tgacacttac aagatggaca gggatgataa ttgggcctcc 180
aagaacaatt ta 192

<210> 52
<211> 194
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v2 alternatively spliced
transcript

<400> 52
cgcgtcgggc tgcaggagaa gatggcggtc tccacaggag ttaaagttcc tcgtaatttt 60
cgcttggttg aagaacttga agaaggacaa aaaggagtag gcgacggtac agttagctgg 120
ggccttgaag atgatgaaga tatgacactt acaaggtgga caggcatgat tattggggcca 180
ccaaggacaa atta 194

<210> 53
<211> 113
<212> DNA
<213> Homo sapiens

<220>
<223> portion of Ubce2v1_2 and Ubce2v1_1 alternatively spliced
transcripts

<400> 53
gaaggccaga aaggagtagg agatggcaca gttagctggg gtctagaaga tgacgaagac 60
atgacactta caagatggac agggatgata attgggcctc caagaacaat tta 113

<210> 54
<211> 49
<212> DNA
<213> Homo sapiens

<220>
<223> portion of G3_2H2 sequence

<400> 54
cgaatatata gccttaaaaat agaatgtgga cctaaatacc cagaagcac 49

<210> 55
 <211> 60
 <212> DNA
 <213> Homo sapiens

<220>
 <223> portion of Ubce2v1, Ubce2v1_2, Ubce2v1_1 and Ubce2v1Bs
 alternatively spliced transcripts

<400> 55
 cgaatatata gccttaaaat agaatgtgga cctaaatacc cagaagcacc cccctttgta 60

<210> 56
 <211> 60
 <212> DNA
 <213> Homo sapiens

<220>
 <223> portion of Ubce2v2 alternatively spliced
 transcript

<400> 56
 agaatatata gcctgaaagt agaatgtgga cctaaatacc cagaagctcc tccgtcagtt 60

<210> 57
 <211> 225
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Uch-13 sequence

<400> 57
 Met Glu Gly Gln Arg Trp Leu Pro Leu Glu Ala Asn Pro Glu Val Thr
 1 5 10 15
 Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val
 20 25 30
 Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro
 35 40 45
 Val Cys Ala Val Leu Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
 50 55 60
 Phe Arg Thr Glu Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val
 65 70 75 80
 Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly
 85 90 95
 Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
 100 105 110
 Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser
 115 120 125
 Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile
 130 135 140

Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro
145 150 155 160

Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val
165 170 175

Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn
180 185 190

His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val
195 200 205

Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala
210 215 220

Ile
225

<210> 58

<211> 231

<212> PRT

<213> Homo sapiens

<220>

<223> portion of BAP-1

<400> 58

Met Asn Lys Gly Trp Leu Glu Leu Glu Ser Asp Pro Gly Leu Phe Thr
1 5 10 15

Leu Leu Val Glu Asp Phe Gly Val Lys Gly Val Gln Val Glu Glu Ile
20 25 30

Tyr Asp Leu Gln Ser Lys Cys Gln Gly Pro Val Tyr Gly Phe Ile Phe
35 40 45

Leu Phe Lys Trp Ile Glu Glu Arg Arg Ser Arg Arg Lys Val Ser Thr
50 55 60

Leu Val Asp Asp Thr Ser Val Ile Asp Asp Asp Ile Val Asn Asn Met
65 70 75 80

Phe Phe Ala His Gln Leu Ile Pro Asn Ser Cys Ala Thr His Ala Leu
85 90 95

Leu Ser Val Leu Leu Asn Cys Ser Ser Val Asp Leu Gly Pro Thr Leu
100 105 110

Ser Arg Met Lys Asp Phe Thr Lys Gly Phe Ser Pro Glu Ser Lys Gly
115 120 125

Tyr Ala Ile Gly Asn Ala Pro Glu Leu Ala Lys Ala His Asn Ser His
130 135 140

Ala Arg Pro Glu Pro Arg His Leu Pro Glu Lys Gln Asn Gly Leu Ser
145 150 155 160

Ala Val Arg Thr Met Glu Ala Phe His Phe Val Ser Tyr Val Pro Ile
165 170 175

Thr Gly Arg Leu Phe Glu Leu Asp Gly Leu Lys Val Tyr Pro Ile Asp
 180 185 190
 His Gly Pro Trp Gly Glu Asp Glu Glu Trp Thr Asp Lys Ala Arg Arg
 195 200 205
 Val Ile Met Glu Arg Ile Gly Leu Ala Thr Ala Gly Glu Pro Tyr His
 210 215 220
 Asp Ile Arg Phe Asn Leu Met
 225 230

<210> 59
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

<400> 59
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly
195 200

<210> 60

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DEAD box
conserved motif

<400> 60

Asp Glu Ala Asp

1